

Paper NO. 34



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/029,042E

DATE: 05/21/2002

TIME: 14:26:46

Input Set : A:\029042e

Output Set: N:\CRF3\05212002\I029042E.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: KIM, Sun-Young
5 KIM, Kee-Won
6 KIM, Tae-Han
7 HWANG, Jeong-Ho
8 KIM, Seon-Hee
9 LEE, Sun-Young

W--> 10 <120> TITLE OF INVENTION: Heterologous Protein Production System using Avian Cells
W--> 11 <140> CURRENT APPLICATION NUMBER: US 09/029,042E
W--> 0 <130> FILE REFERENCE:
12 <141> CURRENT FILING DATE: 1998-05-15
13 <150> PRIOR APPLICATION NUMBER: KR 10-1995-26391
14 <151> PRIOR FILING DATE: 1995-08-24
15 <150> PRIOR APPLICATION NUMBER: PCT/KR96/00145
16 <151> PRIOR FILING DATE: 1996-08-23

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23 <212> TYPE: DNA
24 <213> ORGANISM: erythropoietin(AM)

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The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

see item #10 on Error
Summary Sheet.

paper NO:
34

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Input Set : A:\029042e

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91 <212> TYPE: DNA

92 <213> ORGANISM: erythropoietin(SY)

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103 agaattctcat ttgcgagcct gattttggat gaaagggaga atgatcgagg gaaaggtaaa 600
104 atggagcagc agagatgagg ctgcctgggc gcagaggctc acgtctataa tcccaggctg 660
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PATENT APPLICATION: US/09/029,042E

DATE: 05/21/2002
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Input Set : A:\029042e
Output Set: N:\CRF3\05212002\I029042E.raw

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VERIFICATION SUMMARY

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Input Set : A:\029042e

Output Set: N:\CRF3\05212002\I029042E.raw

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L:161 M:283 W: Missing Blank Line separator, <400> field identifier
L:195 M:283 W: Missing Blank Line separator, <400> field identifier
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Raw Sequence Listing Error Summary .

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>
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SERIAL NUMBER: 09/029, 042E

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

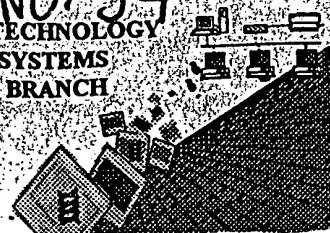
- | | | |
|----|--|--|
| 1 | _____ Wrapped Nucleics
_____ Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 | _____ Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | _____ Misaligned Amino
_____ Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. |
| 4 | _____ Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | _____ Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | _____ PatentIn 2.0
_____ "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | _____ Skipped Sequences
(OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |
| 8 | _____ Skipped Sequences
(NEW RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | _____ Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 10 | _____ Invalid <213>
_____ Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence |
| 11 | _____ Use of <220> | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) |
| 12 | _____ PatentIn 2.0
_____ "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |

R. DEBERRY

YUPPER NO: 34

BIOTECHNOLOGY
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RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/029,042E
Source: 1600
Date Processed by STIC: 5/21/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002